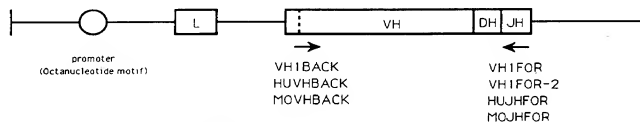




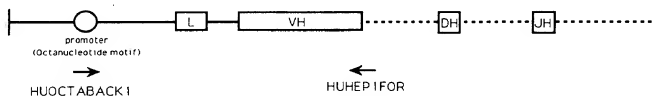
Inventor: Gregory P. WINTER,
et al
SN 09/722,364/Sheet 1 of 23
Atty. Dkt.: 620-122

6545142

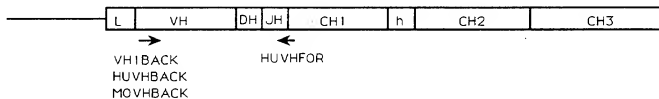
Rearranged heavy chain variable gene (DNA)



Unrearranged heavy chain variable gene (DNA)



Rearranged heavy chain variable gene (mRNA)



Rearranged light chain variable gene (DNA)

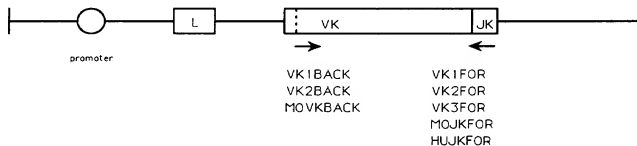


FIG. 1



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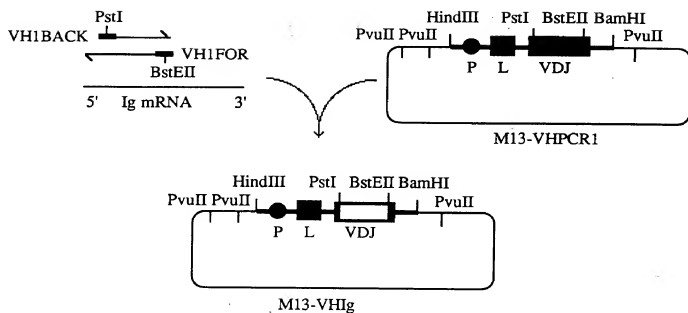


FIG. 2

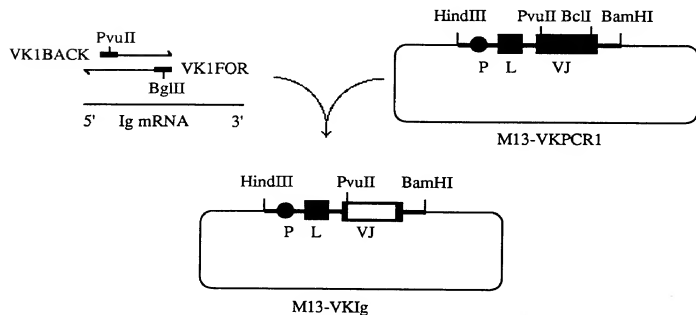


FIG. 4



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M13 VHPCR1

Hind III⁽¹⁾

1
AAGCTTATGAATATGCAAAATCCTCTGAATCTACATGGTAAATATAGGTTGTCTATACCA
10 20 30 40 50 60

CAAAACAGAAAACATGAGATCAGAGTCTCTCTACAGTTACTGAGCACACGACGACCTCAC
70 80 90 100 110 120

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGTATCATCTCTTCTTGGTAGCAACAGCTACAGSTAAGGGGCTCAC
130 140 150 160 170 180

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAATGACATCCACTTTGCCTTTC
190 200 210 220 230 240

PstI
51
10
G V H S 1 Q V Q L Q E S G P G L V R P
TCTCCACAGGGTGTCCACITCCCAGGTCCAACITGCAGGAGAGCGGTCCAGGTCTTGTGAGAC
250 260 270 280 290 300

CDR1
15 20 25 30
S Q T L S L T C T V S G S T F S S Y W M
CTAGCCAGACCTTGAGCCTGACCTGCACCGTGTCTGGCAGCACCTTCAGCAGCTACTGGA
310 320 330 340 350 360

CDR2
35 40 45 50
H W V R Q P P G R G L E W I G R I D P N
TGCACITGGGTGAGACAGCCACCTGGACGAGGTCTTGAGTGGATTGGAAGGATTGATCCTA
370 380 390 400 410 420

55 60 65 70
S G G T K Y N E K F K S R V T M L V D T
ATAGTGGTGTACTAAGTACAATGAGAAGTTCAGAGCAGAGTGACAATGCTGGTAGACA
430 440 450 460 470 480

75 80 85 90
S K N Q F S L R L S S V T A A D T A V Y
CCAGCAAGAACCAGTTACGCTTGAGACTCAGCAGCGTGACAGCCGCGACACCCGGTCTCT
490 500 510 520 530 540

CDR3
95 100 105 110
Y C A R Y D Y Y G S S Y F D Y W G Q G T
ATTATTGTGCAAGATACGATTACTACGGTAGTAGCTACTTTGACTACTGGGCGCAAGGGA
550 560 570 580 590 600

BstEII
115 120
T V T V S S
CCACGGTCCACGCTCTCTCAGGTGAGTCTTACAACCTCTCTCTTCTATTACAGTTAAAT
610 620 630 640 650 660
AGATTTTACTGCATTTGTTGGGGGGGAAATGTGTGTATCTGAATTTTCAGGTTCATGAAGGA
670 680 690 700 710 720
CTAGGGACACCTTGGGAGTCAGAAAGGTCATTGGGAGCCCGGCTGTATGCACAGACAGACA
730 740 750 760 770 780

BamHI
1
TCTCTCAGCTCCACAGACTTCATGGCCAGAGATTTATAG
790 800 810

FIG. 3



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M13 V~~K~~PCR1

Hind III
|
AAGCTTATGAATATGCAAACTCCTCTGAATCTACATGGTAAATATAGGTTGTCTATACCA
38 48 58 68 78 88

CAAACAGAAAAACATGAGATCAGAGTTCTCTCTACAGTTACTGAGCACACAGGACCTCAC
98 108 118 128 138 148

M G W S C I I L F L V A T A T
CATGGAGTGGAGCTGTATCATCTCTCTTGGTAGCAACAGCTACAGGTAAGGGGCTCAC
158 168 178 188 198 208

AGTAGCAGGCTTGAGGTCTGGACATATATATGSGTGACAATGACATCCACTTTGCCTTTC
218 228 238 248 258 268

Pvu II
|
1 5 10
G V H S D I Q L T Q S P S S L S A S
TCTCCACAGGTGTCCTCACTCCGACATCCAGCTGACCCAGAGCCCAAGCAGCGCTGAGCGCCA
278 288 298 308 318 328

CDR1
15 20 25 30
V G D R V T I T C R A S G N I H N Y L A
GCGTGGGTGACAGAGTGACCATCACCTGTAGAGCCAGCGGTAACTCCACAACACTACCTGG
338 348 358 368 378 388

CDR2
35 40 45 50
W Y Q Q K P G K A P K L L I Y Y T T T L
CTTGGTACCAGCAGAGAAGCCAGGTAAAGGCTCCAAGCTGCTGATCTACTACACCACCAACC
398 408 418 428 438 448

55 60 65 70
A D G V P S R F S G S G S G T D F T F T
TGGCTCAGCGGTGTCCTAAGCAGATTACGCGGTAGCGGTAGCGGTACCGACTTCACCTTCA
458 468 478 488 498 508

CDR3
75 80 85 90
I S S L Q P E D I A T Y Y C Q H F W S T
CCATCAGCAGCGCTCCAGCCAGAGACATCGCCACCTACTACTGCCAGCACTTCTGGAGCA
518 528 538 548 558 568

Bcl I (requires dam⁻ host)
|
95 100 105 108
P R T F G Q G T K V V I K R
CCCCAAGGACGTTCTGGCCAAAGGGACCAAGGTGGTGGATCAACCGTAGTAGAATTTAAACT
578 588 598 608 618 628

BamHI
|
TTGCTTCTCTCAGTTGGATCC
638 648

FIG. 5



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Sequence of MBrl VH

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PstI 10 20
Q V Q L O E S G T E L A S P G A S V T L
CAGGTCCAACCTGCAGGAGTCAGGAAGTCTGGCGAGTCTCTGGGCATCAGTGACACTG
VH1BACK SITE

30 CDR1 40
S C K A S' G Y T F T D H I I N W V K K R
TCCTGCAAGGCTTCTGGCTACACATTACTGACCATATTATAAATGGGTAAAAAGAGG
52a 53 CDR2
P G Q G L E W I G R I Y P V S G V T N Y
CCTGGACAGGGCCTTGAGTGGATTGGAAGGATTTATCCAGTAAGTGGTGTAACTAACTAC
60 CDR2 65 70
N O K F M G K A T F S V D R S S N T V Y
AATCAAAAATTCATGGGCAAGGCCACATCTCTGTAGACCGGTCCCTCCAACACAGTGTAC
80 82A B C 83 90 CDR3
M V L N S L T S E D P A V Y Y C G R G F
ATGGTGTGAACAGTCTGACATCTGAGGACCTGCTGTCTATTACTGTGGAAGGGGCTTT
CDR3 103 BstEII Splice
D F D Y W G Q G T T V T V S S ↓
GATTTTGACTACTGGGCGCAAGGGACCAAGCTGTCCTCAGGT.....
VH1FOR SITE

Sequence of MBrl VK

Splice -1
↓ G V H S
AGGTGTCCACTCC

1 PvuII 10 20
D I Q L T Q S P P S L T V T S V G E R V T
GACATTCAGCTGACCCAGTCTCCACCATCCCTGACTGTGTGTCAGTAGGAGGGTCACT
VK1BACK SITE

27A B C D E F CDR1
I S C K S N O N L L W S G N R R Y C L G
ATCAGTTGCAATCCAATCAGAATCTTTTATGGAGTGGAACCGAAGTACTGTGGGC
35 40 50 CDR2
W H Q W K P G Q T P T P L I T W T S D R
TGGCACCAAGTGGAACCAAGGGCAAACTCTACACCGTGTGATCACCTGGACATCTGATAGG
60 70
F S G V P D R F I G S G S V T D F T L T
TTCTCTGGAGTCCCTGATCGTTTCATAGGCAGTGGATCTGTGACAGATTTCACTCTGACC
80 90 CDR3
I S S V Q A E D V A V Y F C Q O H L D L
ATCAGCAGTGTGCAGGCTGAAGATGTGGCAGTTTATTCTGTGACCAACATTTGGACCTT
95 100 BglII/BclI Splice
P Y T F G G G T K L E I K ↓
CCGTACACGTTCCGGAGGGGGGACCAAGCTGGAGATCAAACTGAG
VK1FOR SITE

FIG. 6



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α -Lys 30

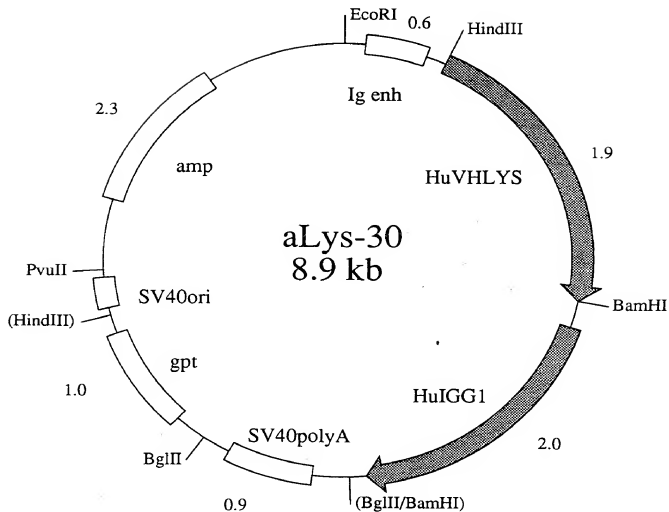


FIG. 7



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α -Lys 17

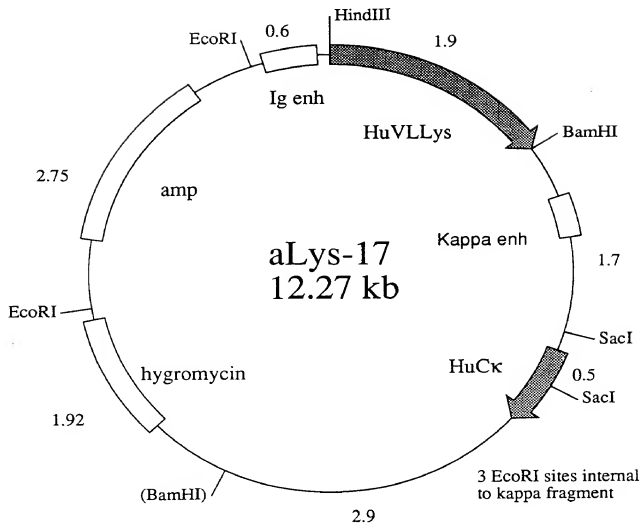


FIG. 8

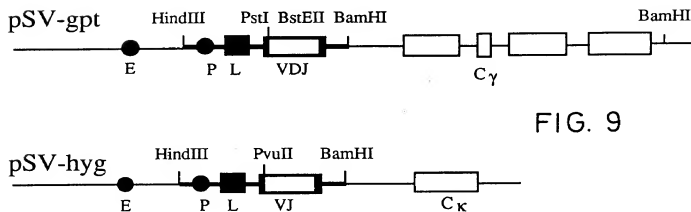


FIG. 9



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FR1**CDR 1****FR2****CDR 2****KABAT IA**

A07 PGLVKPQSLSLTCVSVTGYSIT
A09 PGLVKPQSLSLTCVSVTGYSIT
E03 PGLVKPQSLSLTCVSVTGYSIT
G01 PGLVKPQSLSLTCVSVTGYSIT

SGYYWN
SGYYWI
SGYYWN
SGYYWN

WIRQFPGNKLEWMG
WIRQSPGPKLEWMG
WIRQFPGNKLEWMG
WIRQFPGNKLEWMG

YISYDGSNNYNPSLKN
YITHSGETYNPSLQS
YISYDGSNNYNPSLKN
YISYDGSNNYNPSLKN

KABAT IB

A06 PVLVAPQSLSITCAVSDFSLT
25G07 PGLVQPSQSLITCTVSGFSLT
B03 PGLVAPQSLSITCTVSGFSLT
G03 PGLVQPSQSLITCTVSGFSLT
H09 PVLVAPQSLSITCTVSGFSLT
25C10 PGLVAPQSLSITCTVSGFSLT
A12 PGLVAPQSLSITCTVSGFSLT
A08 PGLVAPQSLSITCTVSGFSLT
25G08 PGLVAPQSLSITCTVSGFSLT
A03 PGLVQPSQSLITCTVSGFSLT
C07 PVLVAPQSLSITCTVSGFSLT
H04 PGLVAPQSLSITCTVSGFSLT

NYGVL
SYGVH
SYGVD
SYGVH
SYGVH
SYVAIS
SYVAIS
SYGVH
SYDVD
SYGVH
SYGVH
SYGVD

WVRQPPGKLEWLW
WVRQSPGKLEWLW
WVRQPPGKLEWLW
WVRQSPGKLEWLW
WVRQPPGKLEWLW
WVRQPPGKLEWLW
WVRQPPGKLEWLW
WVRQSPGKLEWLW
WVRQPPGKLEWLW
WVRQSPGKLEWLW
WVRQPPGKLEWLW
WVRQSPGKLEWLW

VIWAGGISTNYNSALMS
VIVSGGSTDYNAAFIS
VIWGGGSTNYNSALMS
VIVSGGSTDYNAAFIS
VIWAGGISTNYNSALMS
VIWGGGSTNYNSALMS
VIVSGGSTNYNSALMS
VIVSGGSTDYNAAFIS
VIVSGGSTNYNSALMS
VIVSGGSTDYNAAFIS
VIVSGGSTNYNSALMS
VIVSGGSTNYNSALMS

KABAT IIA

E04 PELVRPGVSVKISCKSGSYTFT
H07 PELVRPGVSVKISCKSGSYTFT

DYAMH
DYAMH

WVKQSHAKSLEWIG
WVKQSHAKSLEWIG

VISTYGDASYNQKFKD
VISTYGDASYNQKFKD

KABAT IIB

A02 AELVMPGASVKLSCKASGYTFT
B04 AELVKPGASVKMSCKASGYTFT
C05 AELVKPGASVKLSCKASGYTFT
C09 AELVKPGASVKLSCKASGYTFT
D06 AELVKPGASVKMSCKASGYTFT
D08 PELVKPGASVKLSCKASGYTFT
E07 AELVRPGASVKLSCKASGYTFT
G08 PELVKPGASVKISCKASGYTFT
G10 AELVKPGASVKYSCKASGYTFT
25G09 AELVKPGASVKMSCKASGYTFT
F04 TELVKPGASVKLSCKASGYTFT
H02 AELVKPGASVKLSCKASGYTFT
H01 AELVMPGASVKLSCKASGYTFT
25C05 PELVRGTGSVKMSCKASGYTFT
B01 AELVKPGASVKMSCKASGYTFT
B05 AELVRPGSSVKLSCKASGYTFT
B11 AELVKPGASVKMSCKASGYTFT

SYWMH
SYWIT
SYWMH
SYWMH
SYWIT
SYWMH
DYEHH
DYIN
SYWMH
TYPIE
SYWMH
SYWMH
SYWMH
SYWMH
NYWMK
SYWIT
RUHHM
SYWIT

WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQTPIVHGLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG
WVKQRPGQLEWIG

EIDPDSSTYNYNQKFKG
DIYPGSGSTNYNEKFKS
RIDPNSGGSTKYNEKFKS
EINPNSGGSTNYDEKFKS
DIYPGSGSTNYNEKFKS
EINPNSGGSTNYNEKFKS
AIDPTEGCTAYNQKFKG
WYTPGSGSTNYNEKFKG
RIHPDSSTYNYNQKFKG
NHPNDYDSTYNEKFKG
NINPNSGGSTNYNQKFKG
NIDPDSSETHYNYNQKFKD
EIDPDSSTYNYNQKFKG
QIFPASGSITYYNEHMKD
DIYPGSGSTNYNEKFKS
SETMSDATEYSENFKG
DIYPGSGSTNYNEKFKS

KABAT III A

25G05 GGLVQAWGSLSLSCAASGFTFT
C10 GGLVQPGGSLSLSCAASGFTFT
B07 GGLVQPGGSLSLSCAASGFTFT

DYYMS
DYYMN
DYYMS

WVRQPPGKLEWLW
WVRQPPGKLEWLW
WVRQPPGKLEWLW

FIRNKANGYTTEYSASVKG
LIRNKANGYTTEYSASVKG
LIRNKANGYTTEYSASVKG

KABAT III B

G05 GGLVKPGGSLKLSCAASGFTFS
B12 GGLVQPGGSLKLSCESENYEFP
D04 GGLVQPGGSLRLSCAASGFTFS
D05 GGLVQPGGSLRLSCAASGFTFS
F12 GGLVQPGGSLKLSCESENYEFP
F06 GGLVQPGGSLRLSCAASGFTFS
D02 GGLVQPGGSLKLSCESENYEFP
F09 GGLVKPGGSLKLSCAASGFTFS

DYGMH
SDHMS
SYAMS
SYAMS
SYAMS
SYAMS
SYAMS
SYAMS
SYGMS

WVRQPEKGLEWVA
WVR*****VA
WVA*APGKLEWVS
WVA*APGKLEWVS
WVRQ*PEKRLLEVA
WVA*APGKLEWVS
WVRQSGE*LEVA
WVRQTPDKRLLEWVA

YISSGGSITYYADTVKG
AINSDDGSITYYPTDTHR
AISGSGGSITYYADSVKG
AISGSGGSITYYADSVKG
AINSDDGSITYYPTDTHR
AISGSGGSITYYADSAKG
AINSDDGSITYYPTDTHR
TISGGSITYYPDOSVKG

KABAT III C

E06 GGLVQPGGSMKLSCAASGFTFS

DAWMD

WVRQSPKLEWVA

EIRNKANNHATYAESVKG

KABAT V A

C04 AELVKPGASVKLSCKASGYTFT

EYTHH

WVKQRSGQLEWIG

WFPYPGSGSIKYNEKFKD

FIG. 10a



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FR 3

CDR 3

RISITRDTSKNQFFLKLNSVTTEDTATYYCAR
PISITRETSKNQFFLQLNSVTTEDTAMYYCAG
RISITRDTSKNQFFLQLNSVTTEDTATYYCAR
RISITRDTSKNQFFLKLNSVTTEDTATYYCAR

EGNWDGFAY
DRDKLGPWFAY
DSGSGMDY
VSSGYESMDY

RLSISKDTSKSQVFLKMNSLQDDTAVYYCAK
RLSISKDNKSKSQVFFKMNSLQADDTAIYYCAR
RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAK
RLSISKDNKSKSQVFFKMNSLQADDTAIYYCAR
RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAI
RLSISKDNKSKSQVFLKMNSLQDDTARYYYCAR
RLSISKDNKSKSQVFLKMNSLQDDTARYYYCAR
RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAR
RLSISKDNKSKSQVFFKMNSLQADDTAIYYCAR
RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAK
RLSISKDNKSKSQVFLKMNSLQDDTAMYYCAS

HGDSSGYFDY
NDGY
LGRGYAMDY
KRQDYDGRGYYYAMDY
YYDGSFFAY
EGYFFAY
IYYDGSDDYYAMDY
13 nt.
21 nt.
28 nt.
37 nt.
32 nt.

Ps.gene/Unproducti
Unproductive
Unproductive
Unproductive
Unproductive

KATMTVDKSSSTAYMELARLTSSEDSAVYYCAR
KATMTVDKSSSTAYMELARLTSSEDSAVYYCAR

40 nt.
22 nt.
Unproductive
Unproductive

KATLTVDKSSSTAYMQLSSLTSEDSAVYYCVR
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR
KATLTVDKPSSTAYMQLSSLTSEDSAVYYCAR
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTL
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCTI
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR
KATLTVDTSSTAYMQLSSLTSEDSAVYYCAR
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAI
KATLTVEKSSSTVYELSLRLTSDSASVYYCAR
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAR
KATLTVDKSSSTAYMQLSSLTSEDSAVYYCAP
KAAMAVDTSSTAYMQLSSLTSEDTAVYFCL*
KATLTVDKPSSTAYMQLSSLTSEDSASVYYCAR
KATLTANTSSSTAYMELSLTSEDSAVYYCAR
KATLTVDTSSTSYMQLSSLTSEDSAVYYCAR

RGLTYAMDY
YYSNFDY
PNWDHYYYGMDV
LYYYAMDY
SSGYDY
GAARATNAY
GGFAY
SPMDY
EVPGGFYATDY
MDYYGSSLWFAY
TTVVAFDY
KRQYSTYFDH
TGTEFAY
24 nt.
9 nt.
23 nt.
15 nt.

Ps.gene
Ps.gene/Unproducti
Unproductive
Unproductive
Unproductive

RFTISRDNQSILYLQMNALRAEDSATYYCAR
RFTISRDNQSILYLQMNALRAEDSATYYCAR
RFTISRDNQSILYLQMNALRAEDSATYYCAR

YMLIGAMDY
GYYYDGSYYAMDY
23 nt.

Unproductive

RFTISRDNKNTLYLQMTSLRSEDATAMYYCAR
RFTISRDNKNTLYLQMSLRSEDATAMYYCAR
RFTISRDNKNTLYLQMSLRSEDATAMYYCAD
RFTISRDNKNTLYLQMSLRSEDATAMYYCAK
RFTISRDNKNTLYLQMSLRSEDATAMYYCAR
RFTISRDNKNTLYLQMSLRSEDATAMYYCAR
RFTISRDNKNTLYLQMSLRSEDATAMYYCAR
RFTISRDNKNTLYLQMSLRSEDATAMYYCAR
RFTISRDNKNTLYLQMSLRSEDATAMYYCAR

AKFHLFYDY
REGVVESSLGDDV
RGLHWFDP
PNYGGSPFDY
PPMMPSY
43 nt.
28 nt.
35 nt.

Ps.gene
Ps.gene
Ps.gene
Ps.gene
Ps.gene/Unproducti
Ps.gene/Unproducti
Unproductive

RFTISRDSKSRVYLQMSLRSEDATGYYCTG

30 nt.

Unproductive

KATLTADKSSSTVYMELSLRSEDATAVYFCAK

HEDRDSGGYAMDY

FIG. 10b



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CDR_2

FRAMEWORK_3

CDR_3

KABAT HUMAN VH1

| | | |
|-----------|----------------------------------|----------------|
| | STSTAYMELRSLRSEDVAVYCAR | GEGWDHFDY |
| HAQKFFQG | RVTIRRHKSTSTAYMELSSLRSEDVAVYCAR | GSRYGYDCSGYYYL |
| GYAQKFFQG | RVTMTNRNTSISTATMELSSLRSEDVAVYCAR | LAHFGSGSPVDWFD |

KABAT HUMAN VH2

| | | |
|------------|---------------------------------|------------------|
| KHQLQPSLKS | RVTISVDTSKNQFSLKLSSVTAADVAVYCAR | GGVPPAAIMDV |
| KS | RVTISVDTSKNQFSLKLSSVTAADVAVYCAR | MARYYDFWSGYSAYDY |
| SLKS | RLSISQDTSRNQFSLRLSSVTAADVAVYCAR | HRNWGSPVHFDY |
| | ESTSTAYMELSSLRSEDVAVYCAR | DSYGDYGGHY |

KABAT HUMAN VH3

| | | |
|---------------------|-----------------------------------|--------------------------|
| ISYITSSSSYTNYADSVKG | RFTISRDNAKNSLYLQMNSLRADDTAVYYCAR | DGRFGTYSPSDY |
| SVKG | RFTISRDDSKSIAYLQVNSLKTEDAVYYCTR | TIYYDSSGYPYW |
| YADSVKG | RFTISRDNAKNSLYLQMNSLRADDTAVYYCAR | GIALDAFDI |
| YYADSVRD | RFTISRDNKNTLYLQMNSLRADDTAVYYCAK | 53 NT. UNPROD REARR |
| DSVKG | RFTISRDNAKNSLYLQMNSLRDDEDTAVYYCAR | DHSGTGGGSGSYF |
| VSAISGSGGSGTYADSVKG | RFTISRDNPKNTLYLQMNSLRSEDVAVYCAR | KDNLWFD |
| AVISYDGSNKYYADSVKG | RFTISRDNKNTLYLQMNSLRADDTAVYYCAR | DLGGRGVVVVPAPGGRSIYYGMDV |
| GAVISYDGSNKYYADSVKG | RFTISRDNKNTLYLQMNSLRADDTAVYYCAS | LEGIGTIYYGMDV |
| | AKNSLYLQMNSLRADDTAVYYCVR | DDSSSWPKHFQ |
| QYAASVKG | RFTISRDDSKNSLYLQMNSLNTEDTAVYYCVR | SGVVPYLDY |

KNOWN FAMILY

| | |
|----------|-------------------|
| AVYYCAR | DPRIAARPDYYYYMDV |
| TAMYYCAR | GAEVVEPTARYYYGLNV |

FIG. 11



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| | FR1 | CDR1 | FR2 |
|--------------------------------|---------------------|---------|-----------------|
| | YTFT | SYGIS | WVTTGWTRDLRWGMG |
| | GEKPGSSVKVSCASGYTFT | DYFMN | WMRQAPGQRLWWMG |
| QVQLQEIGPRTGEASETSLICAVSGDSIS | | SGNW*I | WVRQPPGKGLEWIG |
| QVQLQESGPGLVK*SETLSLTCTVSGGSIS | | SYIWS | WIRQPPGKGLEWIG |
| | GYTFT | NYCMH | WVRQDHAQGLEWWMG |
| QVQLQESGPGLVKpSETLSLYCAVSGDSIS | | SGNW*I | WVRQPPGKGLEWIG |
| GPRLGEASETSLTCTVSGGSIS | | SSSYIw | WIRQPPGKGLEWIG |
| QVQLQESGPGLVKpSETLSLTCTVSGGSIS | | SYIWS | WIRQPPGKGLEWIG |
| | LSLICAVSGSIS | SGNW*I | WVRQPPGKGLEWIG |
| | SETLSLTCAVYGGSF | GYIWS | WIRQPPGKGLEWIG |
| QVQLVQSGAEVKKPGASVKVSCASGYTFT | | NYCMH | WVRQVLAQGLEWWMG |
| | SETLSLICAVSGDSIS | SGNW*I | WVRQPPGKGLEWIG |
| SRAQTGEASETSLTCTVSGGSIS | | SSSYIYG | WIRQPPGKGLEWIG |
| | CPLTCTVSGGSVSSGS | YIWS | WIRQPPGKGLEWIG |
| GLVKPSETLSLTCTVSGGSIS | | SYIWS | WIGSPGKGLEWIG |
| | SFETLSLICAVSGDSIS | SGNW*I | WVRQPPGKGLEWIG |
| QVQLVQSGAEVKKPGSSVKVSCASGGTFS | | SYAIS | WVRQAPGQGLEWWMG |
| QVQLQWQAGLLKPKSETLSLTCAVYGGSF | | GYIWS | WIRQPPGKGLEWIG |
| QLQLQESGPGLVKpSETLSLTCTVSGGSIS | | SSSYIYG | WIRQPPGKGLEWIG |
| GPGLVKPSQTLSTCTVSGGSIS | | SGGYIWS | WIRQNPgKGLEWIG |

* indicates stop codon (unsure as sequence remains in frame)
 • sequence terminates due to internal restriction site
 lower case denotes frame shift

| CDR2 | FR3 | CDR3 |
|--------------------|-----------------------------------|-------|
| WISAYNGNTNYAQKLG | RVIMTTDTSTSTAYMELRSLRSDDTAVYYCAR | DTVSS |
| WINAGNGNTKYSQKLG | RVITITRDTASTAYMQLSSLRSEDVAVYYCAR | DTVSS |
| EIHHSNSTYNNPSLKS | RITMSVDTSKNQFYLKLS* | |
| RIYTSNSTYNNPSLKS | RVTISVDTSKNQFSLKLSVTAADTAVYYCAR | DTVSS |
| LVCPSDGSSTSYAQKFOA | RVITITRDTSMSTAYMELSSLRSEDVAVYYCAR | DTVSS |
| EIHHSNSTYNNPSLKS | RITMSVDTSKNQFYLKLS* | |
| EINHSGSTNYNNPSLKS | RVTISVDTSKNQFSLKLS* | |
| YIYSGSTNYNNPSLKS | RVTISVDTSKNQFSLKLS* | |
| EIHHSNSTYNNPSLKS | RITMSVDTSKNQFYLKLS* | |
| EINHSGSTNYNNPSLKS | RVTISVDTSKNQFSLKLSVTAADTAVYYCAR | DTVSS |
| LVCPSDGSSTSYAQKFOA | RVITITRDTSMSTAYMELSSLRSEDVAVYYCAR | DTVSS |
| EIHHSNSTYNNPSLKS | RITMSVDTSKNQFYLKLS* | |
| SIYSGSTNYNNPSLKS | RVITIPVDTSKNQFSLKLS* | |
| YIYSGSTNYNNPSLKS | RVTISVDTSKNQFSLKLSVTAADTAVYYCAR | DTVSS |
| RIYTSNSTYNNPSLKS | RVTMSVDTSKNQFSLKLS* | |
| EIHHSNSTYNNPSLKS | RITMSVDTSKNQFYLKLS* | |
| RIIPILGIANYAQKFOG | RVITITADKSTSTAYMELSSLRSEDVAVYYCAR | DTVSS |
| EINHSGSTNYNNPSLKS | RVTISVDTSKNQFSLKLS* | |
| EINHSGSTNYNNPSLKS | RVTISVDTSKNQFSLKLS* | |
| YIYSGSTNYNNPSLKS | RVTISVDTSKNQFSLKLSVTAADTAVYYCAR | DTVSS |

FIG. 12



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pSW1

HindIII site AAGCTT

GCATGCAAATTCTATTTC AAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAACCTGGGTTCCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCAAGAGCCAAGTTTCTTAAAAATGAACAGCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S SmaI
CAAGGCACCGGTACCGCTCTCCTCATAATAAGAGCTATCCCCGGGCTAAGCTCGAATTC
430 440 450 460 470 480

FIG. 13



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PSW2

HindIII AAGCTT

GCATGCAAATTCTATTTC AAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGCGCCCTCAGAGGCCGTGTCCATCAGATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAACTGGGTTCGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGGTGATGGAACACAGACTATAATTACGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCAAGAGCCAAGTTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S
CAAGGCACCAAGGTACCGTCTCCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
430 440 450 460 470 480

AAATTCTATTTC AAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGA
490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGTCCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

S L S A S V G E T V T I T C R A S G N I
TCCCTTTCTGCGTCTGTGGGAGAACTGTCACCATCAGATGTCGAGCAAGTGGGAATATT
610 620 630 640 650 660

H N Y L A W Y Q Q K Q G K S P Q L L V Y
CACAAATTATTAGCATGGGTATCAGCAGAAACAGGGAATCTCCTCAGCTCCTGGTCTAT
670 680 690 700 710 720

FIG. 14 a



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Y T T T L A D G V P S R F S G S G S G T
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTTGGAGTACTCTCGGACGTTCCGTTGGAGGCCAAGCTGGAATCAAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 14 b

pSW1HPOLMYC

HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAATTCATTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

Polylinker
TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

MYC PEPTIDE
V T V S S E O K L I S E E D L N * *
GGTCACCGTCTCCTCAGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAAGCTCGAATTC

FIG. 15



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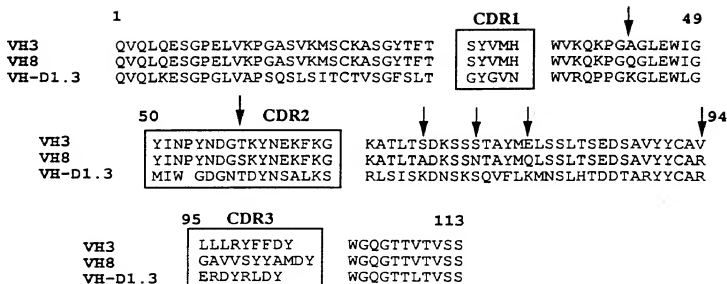


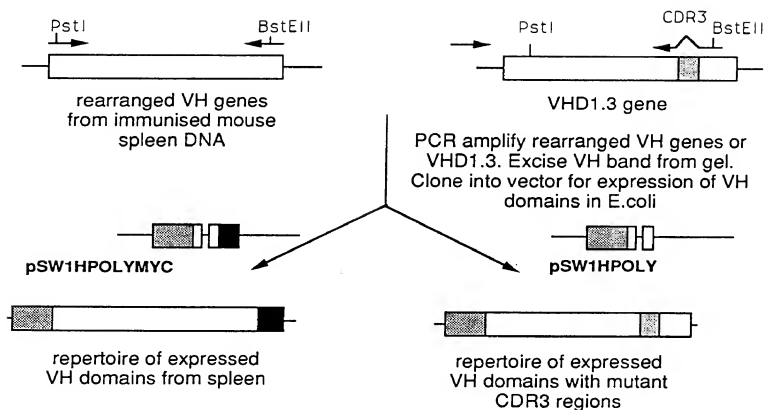
FIG. 16



FIG. 17



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Assay for binding to antigen

FIG. 18



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PSW2HPOLY

HindIII AAGCTT

GCATGCAAAATTTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCTTACGGCAGCC
10 20 30 40 50 60

AGLLLLAQAAMAAQVQLQ
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCCAAGGTGCAGCTGCAG
70 80 90 100 110 PstI

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

VTVSS
GGTCACCGTCTCCTCATAATAAGAGCTCGAATTCGCCAAGCTTGCATGC
BstEII 430 440 450 460 470 480

MAATTTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCTTACGGCAGCCGCTGGA
490 500 510 520 530 540

LLLLAQAAMADIVLTQSPA
TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGACATCGTCTGACTCAGTCTCCAGCC
550 560 570 580 590 600

SLSSASVGETVTITCRASGNIT
TCCCTTTCTGCGTCTGTGGGAGAACTGTCACCATCACATGTCGAGCAAGTGGGAATATT
610 620 630 640 650 660

HNYYLAWYQQKQKSPQLLVY
CACAATTATTAGCATGGTATCAGCAGAAACAGGGAAATCTCCTCAGCTCCTGGTCTAT
670 680 690 700 710 720

YTTTTLADGVPSRFSGSGSGT
TATACAACAACCTTAGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

QYSLKINSLQPEDFGSY Y C Q
CAATATTCCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

HFWSSTPRTFGGGTKLEIKR
CATTTTGGAGTACTCCTCGGACGTTGCGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTC
910

FIG. 19



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M K Y L L P T
AAGCTTGCATGCAAAATCTATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACG
10 20 30 40 50 60
A A A G L L L L A A Q P A M A Q V Q L Q
GCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAG
70 80 90 100 110 120
E S G P G L V A P S Q S L S I T C T V S
GAGTCAGGACCTGGCCTGGTGGCGCCCTCACAGAGCCTGTCCATCATATGCACCGTCTCA
130 140 150 160 170 180
G F S L T G Y G V N W V R Q P P G K G L
GGGTTCTCATTAAACGGCTATGGTGTAACCTGGGTTGCCAGCCTCCAGGAAAGGGTCTG
190 200 210 220 230 240
E W L G M I W G D G N T D Y N S A L K S
GAGTGGCTGGGAATGATTGGGGTGATGGAAACACAGACTATAATTACAGTCTCAAAATCC
250 260 270 280 290 300
R L S I S K D N S K S Q V F L K M N S L
AGACTGAGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTG
310 320 330 340 350 360
H T D D T A R Y Y C A R E R D Y R L D Y
CACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTAC
370 380 390 400 410 420
W G Q G T T V T V S S G G G A P A A A P
TGGGGCCAAGGCCACACCGTCTCCTCAGGTGGTGCTCCAGCAGCTGCACCT
430 440 450 460 470 480
A G G G Q V Q L K E S G P G L V A P S Q
GCTGGAGGAGACAGGTGCAGCTGAAGGAGTCAGGACCTGGCCTGGTGGCGCCCTCACAG
490 500 510 520 530 540
S L S I T C T V S G F S L T G Y G V N W
AGCCTGTCCATCATATGCACCGTCTCAGGGTTCTCATTAAACCGGCTATGGTGTAACTGG
550 560 570 580 590 600
V R Q P P G K G L E W L G M I W G D G N
GTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGTATGGAAC
610 620 630 640 650 660
T D Y N S A L K S R L S I S K D N S K S
ACAGACTATAATTACAGTCTCAAATCCAGACTGAGCATCAGCAAGGACAACCTCCAAGAGC
670 680 690 700 710 720
Q V F L K M N S L H T D D T A R Y Y C A
CAAGTTTCTTAAAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTGTGGC
730 740 750 760 770 780
R E R D Y R L D Y W G Q G T T V T V S S
AGAGAGAGATTATAGGCTTGACTACTGGGGCCAAGGCCACCGTCACTGCTCCTCA
790 800 810 820 830 840
* *
TAATAAGAGCTC
850

FIG. 20



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M K Y L L P T A A
GCATGCAAAATTCATTTCAAGGAGACAGTCATATGAAATACCTATTGCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCGTGGTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGTTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAACATGGGTTCGCCAGCCTCCAGGAAAGGCTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGGTGATGGAACACAGACTATAATTACGCTCTCAAATCCAGCTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACTCCAAAGCCAAAGTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S R T P E M P V L E N R
CAAGGCACCCAGGTACCGCTCTCCTCACGGACACCAGAAATGCCTGTTCTGGAACCCGG
430 440 450 460 470 480

A A Q G D I T A P G G A R R L T G D Q T
GCTGCTCAGGGCGATATTACTGCACCCGGCGGTGCTCGCCGTTTAAACGGGTGATCAGACT
490 500 510 520 530 540

A A L R D S L S D K P A K N I I L L I G
GCCGCTCTGGGTGATCTCTTAGCGATAAACCTGCAAAAAATATTATTTTGTGATGGC
550 560 570 580 590 600

D G M G D S E I T A A R N Y A E G A G G
GATGGGATGGGGACTCGGAAATTAAGTCCCGCACGTAATTATGCCGAAGGTGCGGGCGGC
610 620 630 640 650 660

F F K G I D A L P L T G Q Y T H Y A L N
TTTTTTAAAGGTATAGATGCTTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
670 680 690 700 710 720

K K T G K P D Y V T D S A A S A T A W S
AAAAAACCGGCAACCGGACTACGTACCGGACTCGGCTGCATCAGCAACCGCTGGTCA
730 740 750 760 770 780

FIG. 21a



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T G V K T Y N G A L G V D I H E K D H P
ACCGGTGTGCAAAACCTATAACGGCGCGCTGGCGTCGATATTACGAAAAAGATCACCCA
790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
ACGATTCTGGAATGCGAAAAAGCCGAGGTCTGGCGACCGGTAACGTTTCTACCGCAGAG
850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
TTGCAGGATGCCACGCCCGCTGCGCTGGTGGCACATGTGACCTCGCGCAATGCTACGGT
910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
CCGAGCGCGACCAAGTAAAAATGTCCGGGTAAACGCTCTGGAAAAAGCGGAAAAAGGATCG
970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
ATTACCGAACAGTGCTTAACGCTCGTGCCGACGTTACGCTTGGCGCGCGCAAAACCC
1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
TTTGCTGAACCGCAACCGCTGGTGAATGGCAGGAAAAACGCTGCGTGAACAGGCACAG
1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
GCGCGTGGTTATCAGTTGGTGAGCGATGCTGCCTCACTGAATTCGGTGACGGAAGCGAAT
1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
CAGCAAAAAACCCCTGCTTGGCCTGTTTGCTGACGGCAATATGCCAGTGCGCTGGCTAGGA
1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG
1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
CAACGTAATGACAGTGTACCAACCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG
1330 1340 1350 1360 1370 1380

S K N E K G F F L Q V E G A S I D K Q D
AGTAAAAATGAGAAAGGCTTTTCTCTGCAAGTTGAAGTGCGTCAATCGATAACAGGAT
1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
CATGCTGCGAATCCTTGTGGGCAAATTGGCGAGACGGTCGATCTCGATGAAGCCGTACAA
1450 1460 1470 1480 1490 1500

R A L E F A K K E G N T L V I V T A D H
CGGGCGCTGGAATTCGCTAAAAAGGAGGTAACACGCTGGTCATAGTCACCGCTGATCAC
1510 1520 1530 1540 1550 1560

FIG. 21b



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A H A S Q I V A P D T K A P G L T Q A L
GCCCACGCCAGCCAGATTGTTGCGCCGGATACCAAAGCTCCGGGCCTCACCCAGGCGCTA
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
AATACCAAAGATGGCGCAGTGATGGTGATGAGTTACGGGAACCTCCGAAGAGGATTCACAA
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A N V V
GAACATACCGGCAGTCAGTTGCGTATTGCGGCGTATGGCCCGCATGCCGCCAATGTTGTT
1690 1700 1710 1720 1730 1740

G L T D O T D L F Y T M K A A L G L K *
GGACTGACCGACCAGACCGATCTCTTCTACACCATGAAAGCCGCTCTGGGGCTGAAATAA
1750 1760 1770 1780 1790 1800

AACCGCGCCCGGGAGTGAATTTTCGCTGCCGGGTGGTTTTTTTGCTGTTAGC
1810 1820 1830 1840 1850

FIG. 21c



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GCATGCAAATTCTATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

M K Y L L P T A A
A G L L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCAACCAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCCTGGTGGCGCCTCACAGAGCCTGTCCATGCACCGCTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGCTATGGTGTAACTGGGTTCGCCAGCCTCCAGGAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTGGGGTGATGGAACACAGACTATAATTCAGCTCTCAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAAGAGCCAAGTTTCTTAAAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATTATAGGCTTGACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S * *
CAAGGCACCCAGGTCACCGTCTCCTCATAATAAGAGCTATCCCGGGAGCTTGCATGCAAA
430 440 450 460 470 480

M K Y L L P T A A A G L
TTCTATTTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
490 500 510 520 530 540

L L L A A Q P A M A D I E L V D L E I K
TTATTACTCGCTGCCAACCAGCGATGGCCGACATCGAGCTCGTCGACCTCGAGATCAAA
550 560 570 580 590 600

R E Q K L I S E E D L N * *
CGGGAACAAAACTCATCTCAGAAGAGGATCTGAATTAATGATCAAACGGTAATAAG
610 620 630 640 650 660

GATCCAGCTCGAATTC
670

FIG. 22



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Q V Q L Q E S G P G L V Q P S Q S L S I
CAGGTGCAGCTGCAGGAGCTCAGGACCTGGCCTAGTGCAGCCCTCACAGAGCCTGTCCATC
10 20 30 40 50 60
T C T V S G F S L T S Y G V H W V R Q S
ACCTGCACAGTCTCTGGTTTCTCATTAACTAGCTATGGTGTACACTGGGTTCGCCAGTCT
70 80 90 100 110 120
P G K G L E W L G M I W G D G N T D Y N
CCAGGAAAGGGTCTGGAGTGGCTGGGAATGATTGGGGTGATGGAACACAGACTATAAT
130 140 150 160 170 180
S A L K S R L S I S K D N S K S Q V F L
TCAGTCTCTCAATCCAGACTGAGCATCAGCAAGGACAACCTCCAGAGCCAAGTTTCTTA
190 200 210 220 230 240
K M N S L H T D D T A R Y Y C A R E R D
AAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTGTGCCAGAGAGAGAT
250 260 270 280 290 300
Y R L D Y W G Q G T T V T V S S
TATAGGCTTGACTACTGGGGCCAAGGGACCCAGGTCCACCGTCTCCTCA
310 320 330 340

FIG. 23